



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Kaufman, Randal J.
Wasley, Louise

(ii) TITLE OF INVENTION: Method of Increasing Yield of
Mature Proteins

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genetics Institute, Inc.
(B) STREET: 87 CambridgePark Drive
(C) CITY: Cambridge
(D) STATE: Massachusetts
(E) COUNTRY: United States of America
(F) ZIP: 02140

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb storage
(B) COMPUTER: IBM PS/2
(C) OPERATING SYSTEM: PC-DOS
(D) SOFTWARE: WordPerfect 5.1

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA: not applicable

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: GI 5181

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(2) INFORMATION FOR SEQ ID NO:1

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2385 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: partial human genomic DNA

(A) DESCRIPTION: sequence encoding furin

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v) PUBLICATION INFORMATION:

(A) AUTHORS: van den Ouweland, A. M. W.
(B) JOURNAL: Nucl. Acids. Res.
(C) VOLUME: 18
(D) PAGES: 664
(E) DATE: 1990

(vi) SEQUENCE DESCRIPTION: SEQ ID NO:1

ATG GAG CTC AGG CCC TGG TTC	21
Met Glu Leu Arg Pro Trp Leu	
1 5	
CTA TGG GTC GTA CCA CCA ACA GGA ACC TTG GTC CTG CTA	60
Leu Trp Val Val Ala Ala Thr Gly Thr Leu Val Leu Leu	
10 15 20	
GCA GCT GAT GCT CAG GGC CAG AAG GTC TTC ACC AAC ACG	99
Ala Ala Asp Ala Gln Gly Gln Lys Val Phe Thr Asn Thr	
25 30	
TGG GCT GTG CGC ATC CCT GGA GGC CCA GCG GTG GCC AAC	138
Trp Ala Val Arg Ile Pro Gly Gly Pro Ala Val Ala Asn	
35 40 45	
AGT GTG GCA CGG AAG CAT GGG TTC CTC AAC CTG GGC CAG	177
Ser Val Ala Arg Lys His Gly Phe Leu Asn Leu Gly Gln	
50 55	

ATC	TTC	GGG	GAC	TAT	TAC	CAC	TTC	TGG	CAT	CGA	GGA	GTG	216
Ile	Phe	Gly	Asp	Tyr	Tyr	His	Phe	Trp	His	Arg	Gly	Val	
60					65					70			
ACG	AAG	CGG	TCC	CTG	TCG	CCT	CAC	CGC	CCG	CGG	CAC	AGC	255
Thr	Lys	Arg	Ser	Leu	Ser	Pro	His	Arg	Pro	Arg	His	Ser	
		75					80					85	
CGG	CTG	CAG	AGG	GAG	CCT	CAA	GTA	CAG	TGG	CTG	GAA	CAG	294
Arg	Leu	Gln	Arg	Glu	Pro	Gln	Val	Gln	Trp	Leu	Glu	Gln	
				90					95				
CAG	GTG	GCA	AAG	CGA	CGG	ACT	AAA	CGG	GAC	GTG	TAC	CAG	333
Gln	Val	Ala	Lys	Arg	Arg	Thr	Lys	Arg	Asp	Val	Tyr	Gln	
	100					105					110		
GAG	CCC	ACA	GAC	CCC	AAG	TTT	CCT	CAG	CAG	TGG	TAC	CTG	372
Glu	Pro	Thr	Asp	Pro	Lys	Phe	Pro	Gln	Gln	Trp	Tyr	Leu	
			115					120					
TCT	GGT	GTC	ACT	CAG	CGG	GAC	CTG	AAT	GTG	AAG	GCG	GCC	411
Ser	Gly	Val	Thr	Gln	Arg	Asp	Leu	Asn	Val	Lys	Ala	Ala	
125					130					135			
TGG	GCG	CAG	GGC	TAC	ACA	GGG	CAC	GGC	ATT	CTG	GTC	TCC	450
Trp	Ala	Gln	Gly	Tyr	Thr	Gly	His	Gly	Ile	Val	Val	Ser	
		140					145					150	
ATT	CTG	GAC	GAT	GGC	ATC	GAG	AAG	AAC	CAC	CCC	GAC	TTG	489
Ile	Leu	Asp	Asp	Gly	Ile	Glu	Lys	Asn	His	Pro	Asp	Leu	
				155					160				
GCA	GGC	AAT	TAT	GAT	CCT	GGG	GCC	AGT	TTT	CAT	GTC	AAT	528
Ala	Gly	Asn	Tyr	Asp	Pro	Gly	Ala	Ser	Phe	Asp	Val	Asn	
	165					170					175		
GAC	CAG	GAC	CCT	GAC	CCC	CAG	CCT	CGG	TAC	ACA	CAG	ATG	567
Asp	Gln	Asp	Pro	Asp	Pro	Gln	Pro	Arg	Tyr	Thr	Gln	Met	
			180					185					
AAT	GAC	AAC	AGG	CAC	GGC	ACA	CGG	TGT	GCG	GGG	GAA	GTG	606
Asn	Asp	Asn	Arg	His	Gly	Thr	Arg	Cys	Ala	Gly	Glu	Val	
190					195					200			
GCT	GCC	GTG	GCC	AAC	AAC	CGT	GTC	TGT	GGT	GTA	GGT	GTG	645
Ala	Ala	Val	Ala	Asn	Asn	Gly	Val	Cys	Gly	Val	Gly	Val	
		205				210						215	
GCC	TAC	AAC	GCC	CGC	ATT	GGA	GGG	GTC	CGC	ATG	CTG	GAT	684
Ala	Tyr	Asn	Ala	Arg	Ile	Gly	Gly	Val	Arg	Met	Leu	Asp	
				220					225				

GGC Gly 230	GAG Glu 230	GTG Val 230	ACA Thr 230	GAT Asp 230	GCA Ala 235	GTG Val 235	GAG Glu 235	GCA Ala 235	CGC Arg 235	TCG Ser 235	CTG Leu 240	GGC Gly 240	723
CTG Leu 245	AAC Asn 245	CCC Pro 245	AAC Asn 245	CAC His 245	ATC Ile 245	CAC His 250	ATC Ile 250	TAC Tyr 250	AGT Ser 250	GCC Ala 250	AGC Ser 250	TGG Trp 250	762
GGC Gly 255	CCC Pro 255	GAG Glu 255	GAT Asp 255	GAC Asp 260	GGC Gly 260	AAG Lys 260	ACA Thr 260	GTG Val 260	GAT Asp 265	GGG Gly 265	CCA Pro 265	GCC Ala 265	801
CGG Arg 270	CTC Leu 270	GCC Ala 270	GAG Glu 270	GAG Glu 270	GCC Ala 270	TTC Phe 275	TTC Phe 275	CGT Arg 275	GGG Gly 275	CTT Val 275	AGC Ser 280	CAG Gln 280	840
GGC Gly 285	CGA Arg 285	GGG Gly 285	GGG Gly 285	CTG Leu 285	GGC Gly 285	TCC Ser 285	ATC Ile 285	TTT Phe 290	GTC Val 290	TGG Trp 290	GCC Ala 290	TCG Ser 290	879
GGG Gly 295	AAC Asn 295	GGG Gly 295	GGG Gly 295	CGG Arg 295	GAA Glu 300	CAT His 300	GAC Asp 300	AGC Ser 300	TGC Cys 300	AAC Asn 305	TGC Cys 305	GAC Asp 305	918
GGC Gly 310	TAC Tyr 310	ACC Thr 310	AAC Asn 310	AGT Ser 310	ATC Ile 310	TAC Tyr 315	ACG Thr 315	CTG Leu 315	TCC Ser 315	ATC Ile 315	AGC Ser 315	AGC Ser 315	957
GCC Ala 320	ACG Thr 320	CAG Gln 320	TTT Phe 320	GGC Gly 325	AAC Asn 325	GTG Val 325	CCG Pro 325	TGG Trp 325	TAC Tyr 330	AGC Ser 330	GAG Glu 330	GCC Ala 330	996
TGC Cys 335	TCG Ser 335	TCC Ser 335	ACA Thr 335	CTG Leu 335	GCC Ala 340	ACG Thr 340	ACC Thr 340	TAC Tyr 340	AGC Ser 340	AGT Ser 340	GGC Gly 345	AAC Asn 345	1035
CAG Gln 350	AAT Asn 350	GAG Glu 350	AAG Lys 350	CAG Gln 350	ATC Ile 350	GTG Val 355	ACG Thr 355	ACT Thr 355	GAC Asp 355	TTG Leu 355	CGG Arg 355	CAG Gln 355	1074
AAG Lys 360	TGC Cys 360	ACG Thr 360	GAG Glu 360	TCT Ser 360	CAC His 365	ACG Thr 365	GGC Gly 365	ACC Thr 365	TCA Ser 365	GCC Ala 370	TCT Ser 370	GCC Ala 370	1113
CCC Pro 375	TTA Leu 375	GCA Ala 375	GCC Ala 375	GGC Gly 375	ATC Ile 375	ATT Ile 380	GCT Ala 380	CTC Leu 380	ACC Thr 380	CTG Leu 380	GAG Glu 380	GCC Ala 380	1152
AAT Asn 385	AAG Lys 385	AAC Asn 385	CTC Leu 385	ACA Thr 385	TGG Trp 390	CGG Arg 390	GAC Asp 390	ATG Met 390	CAA Gln 395	CAC His 395	CTG Leu 395	GTG Val 395	1191
GTA Val 1230	CAG Gln 1230	ACC Thr 1230	TCG Ser 1230	AAG Lys 1230	CCA Pro 1230	GCC Ala 1230	CAC His 1230	CTC Leu 1230	AAT Asn 1230	GCC Ala 1230	AAC Asn 1230	GAC Asp 1230	1230

400					405					410					
TGG	GCC	ACC	AAT	GGT	GTG	GGG	CGG	AAA	GTG	AGC	CAC	TCA	1269		
Trp	Ala	Thr	Asn	Gly	Val	Gly	Arg	Lys	Val	Ser	His	Ser			
				415					420						
TAT	GGC	TAC	GGG	CTT	TTC	GAC	GCA	GGC	GCC	ATG	GTG	GCC	1308		
Tyr	Gly	Tyr	Gly	Leu	Leu	Asp	Ala	Gly	Ala	Met	Val	Ala			
	425					430					435				
CTG	GCC	CAG	AAT	TGG	ACC	ACA	GTC	GCC	CCC	CAG	CGG	AAG	1347		
Leu	Ala	Gln	Asn	Trp	Thr	Thr	Val	Ala	Pro	Gln	Arg	Lys			
			440					445							
TGC	ATC	ATC	GAC	ATC	CTC	ACC	GAG	CCC	AAA	GAC	ATC	GGG	1386		
Cys	Ile	Ile	Asp	Ile	Leu	Thr	Glu	Pro	Lys	Asp	Ile	Gly			
450					455					460					
AAA	CGG	CTC	GAC	CTC	CGG	AAC	ACC	GTG	ACC	GCG	TCC	CTG	1425		
Lys	Arg	Leu	Glu	Val	Arg	Lys	Thr	Val	Thr	Ala	Cys	Leu			
		465				470						475			
GGC	GAG	CCC	AAC	CAC	ATC	ACT	CGG	CTG	GAG	CAC	GCT	CAG	1464		
Gly	Glu	Pro	Asn	His	Ile	Thr	Arg	Leu	Glu	His	Ala	Gln			
				480					485						
GCG	CGG	CTC	ACC	CTG	TCC	TAT	AAT	CGC	CGT	GGC	GAC	CTG	1503		
Ala	Arg	Leu	Thr	Leu	Ser	Tyr	Asn	Arg	Arg	Gly	Asp	Leu			
	490					495					500				
GCC	ATC	CAC	CTG	GTC	AGC	CCC	ATG	GGC	ACC	CGC	TCC	ACC	1542		
Ala	Ile	His	Leu	Val	Ser	Pro	Met	Gly	Thr	Arg	Ser	Thr			
			505					510							
CTG	CTG	GCA	GCC	AGG	CCA	CAT	GAC	TAC	TCC	GCA	GAT	GGG	1581		
Leu	Leu	Ala	Ala	Arg	Pro	His	Asp	Tyr	Ser	Ala	Asp	Gly			
515					520					525					
TTT	AAT	GAC	TGG	GCC	TTC	ATG	ACA	ACT	CAT	TCC	TGG	GAT	1620		
Phe	Asn	Asp	Trp	Ala	Phe	Met	Thr	Thr	His	Ser	Trp	Asp			
		530					535					540			
GAC	GAT	CCC	TCT	GGG	GAG	TGG	GTC	CTA	GAG	ATT	GAA	AAC	1659		
Glu	Asp	Pro	Ser	Gly	Glu	Trp	Val	Leu	Glu	Ile	Glu	Asn			
				545					550						
ACC	AGC	GAA	GCC	AAC	AAC	TAT	GGG	ACG	CTG	ACC	AAC	TCC	1698		
Thr	Ser	Glu	Ala	Asn	Asn	Tyr	Gly	Thr	Leu	Thr	Lys	Phe			
	555					560					565				
ACC	CTC	GTA	CTC	TAT	GGC	ACC	GCC	CCT	GAC	GGG	CTC	CCC	1737		
Thr	Leu	Val	Leu	Tyr	Gly	Thr	Ala	Pro	Glu	Gly	Leu	Pro			
			570					575							

GTA	CCT	CCA	GAA	AGC	AGT	GGC	TGC	AAG	ACC	CTC	ACG	TCC	1776
Val	Pro	Pro	Glu	Ser	Ser	Gly	Cys	Lys	Thr	Leu	Thr	Ser	
580					585					590			
AGT	CAG	GCC	TGT	GTG	GTG	TGC	GAG	GAA	GGC	TTC	TCC	CTC	1815
Ser	Gln	Ala	Cys	Val	Val	Cys	Glu	Glu	Gly	Phe	Ser	Leu	
		595					600					605	
CAC	CAG	AAG	AGC	TGT	GTC	CAG	CAC	TGC	CCT	CCA	GGC	TTC	1854
His	Gln	Lys	Ser	Cys	Val	Gln	Asn	Cys	Pro	Pro	Gly	Phe	
				610					615				
GCC	CCC	CAA	GTC	CTC	GAT	ACG	CAC	TAT	AGC	ACC	GAG	AAT	1893
Ala	Pro	Gln	Val	Leu	Asp	Thr	Asn	Tyr	Ser	Thr	Glu	Asn	
	620					625					630		
GAC	GTG	GAG	ACC	ATC	CGG	GCC	AGC	GTC	TGC	GCC	CCC	TGC	1932
Asp	Val	Glu	Thr	Ile	Arg	Ala	Ser	Val	Cys	Ala	Pro	Cys	
			635					640					
CAC	GCC	TCA	TGT	GCC	ACA	TGC	CAG	GGG	CCG	GCC	CTG	ACA	1971
His	Ala	Ser	Cys	Ala	Thr	Cys	Gln	Gly	Pro	Ala	Leu	Thr	
	645				650					655			
GAC	TGC	CTC	AGC	TGC	CCC	AGC	CAC	GCC	TCC	TTG	GAC	CCT	2010
Asp	Cys	Leu	Ser	Cys	Pro	Ser	His	Ala	Ser	Leu	Asp	Pro	
		660					665					670	
GTG	GAG	CAG	ACT	TGC	TCC	CGG	CAA	AGC	CAG	AGC	AGC	CGA	2049
Val	Glu	Gln	Thr	Cys	Ser	Arg	Gln	Ser	Gln	Ser	Ser	Arg	
				675					680				
GAG	TCC	CCG	CCA	CAG	CAG	CAG	CCA	CCT	CGG	CTG	CCC	CCG	2088
Glu	Ser	Pro	Pro	Gln	Gln	Gln	Pro	Pro	Arg	Leu	Pro	Pro	
	685					690					695		
GAG	GTG	GAG	GCG	GGG	CAA	CGG	CTG	CGG	GCA	GGG	CTG	CTG	2127
Glu	Val	Glu	Ala	Gly	Gln	Arg	Leu	Arg	Ala	Gly	Leu	Leu	
			700				705						
CCC	TCA	CAC	CTG	CCT	GAG	GTG	GTG	GCC	GGC	CTC	AGC	TGC	2166
Pro	Ser	His	Leu	Pro	Glu	Val	Val	Ala	Gly	Leu	Ser	Cys	
					715					720			
GCC	TTC	ATC	GTG	CTG	GTC	TTC	GTC	ACT	GTC	TTC	CTG	CTC	2205
Ala	Phe	Ile	Val	Leu	Val	Phe	Val	Thr	Val	Phe	Leu	Val	
		725					730					735	
CTG	CAG	CTG	CGC	TCT	GGC	TTT	AGT	TTT	CGG	GGG	GTG	AAG	2244
Leu	Gln	Leu	Arg	Ser	Gly	Phe	Ser	Phe	Arg	Gly	Val	Lys	
				740					745				
GTG	TAC	ACC	ATG	GAC	CGT	GGC	CTC	ATC	TCC	TAC	AAG	GGG	2283
Val	Tyr	Thr	Met	Asp	Arg	Gly	Leu	Ile	Ser	Tyr	Lys	Gly	

750		755		760									
CTG	CCC	CCT	GAA	GCC	TGG	CAG	GAG	GAG	TGC	CCG	TCT	GAC	2322
Leu	Pro	Pro	Glu	Ala	Trp	Gln	Glu	Glu	Cys	Pro	Ser	Asp	
			765				770						
TCA	GAA	GAG	GAC	GAG	GGC	CGG	GGC	GAG	AGG	ACC	GCC	TTT	2361
Ser	Glu	Glu	Asp	Glu	Gly	Arg	Gly	Glu	Arg	Thr	Ala	Phe	
775					780					785			
ATC	AAA	GAC	CAG	AGC	GCC	CTC	TGA						2385
Ile	Lys	Asp	Gln	Ser	Ala	Leu	End						
			790										

(3) INFORMATION FOR SEQ ID NO:2

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 794 amino acids

(B) TYPE: amino acids

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: furin

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v) PUBLICATION INFORMATION:

(A) AUTHORS: van den Ouweland, A. M. W.

(B) JOURNAL: Nucl. Acids. Res.

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(E) DATE: 1990

(vi) SEQUENCE DESCRIPTION: SEQ ID NO:2

Met Glu Leu Arg Pro Trp Leu
1 5

Leu Trp Val Val Ala Ala Thr Gly Thr Leu Val Leu Leu
10 15 20

Ala Ala Asp Ala Gln Gly Gln Lys Val Phe Thr Asn Thr
25 30

Trp Ala Val Arg Ile Pro Gly Gly Pro Ala Val Ala Asn

35	40	45
Ser Val Ala Arg Lys His Gly Phe Leu Asn Leu Gly Gln		
	50	55
Ile Phe Gly Asp Tyr Tyr His Phe Trp His Arg Gly Val		
60	65	70
Thr Lys Arg Ser Leu Ser Pro His Arg Pro Arg His Ser		
	75	80
		85
Arg Leu Gln Arg Glu Pro Gln Val Gln Trp Leu Glu Gln		
	90	95
Gln Val Ala Lys Arg Arg Thr Lys Arg Asp Val Tyr Gln		
100	105	110
Glu Pro Thr Asp Pro Lys Phe Pro Gln Gln Trp Tyr Leu		
	115	120
Ser Gly Val Thr Gln Arg Asp Leu Asn Val Lys Ala Ala		
125	130	135
Trp Ala Gln Gly Tyr Thr Gly His Gly Ile Val Val Ser		
	140	145
		150
Ile Leu Asp Asp Gly Ile Glu Lys Asn His Pro Asp Leu		
	155	160
Ala Gly Asn Tyr Asp Pro Gly Ala Ser Phe Asp Val Asn		
165	170	175
Asp Gln Asp Pro Asp Pro Gln Pro Arg Tyr Thr Gln Met		
	180	185
Asn Asp Asn Arg His Gly Thr Arg Cys Ala Gly Glu Val		
190	195	200
Ala Ala Val Ala Asn Asn Gly Val Cys Gly Val Gly Val		
	205	210
		215
Ala Tyr Asn Ala Arg Ile Gly Gly Val Arg Met Leu Asp		
	220	225
Gly Glu Val Thr Asp Ala Val Glu Ala Arg Ser Leu Gly		
230	235	240
Leu Asn Pro Asn His Ile His Ile Tyr Ser Ala Ser Trp		
	245	250
Gly Pro Glu Asp Asp Gly Lys Thr Val Asp Gly Pro Ala		
255	260	265

Arg	Leu	Ala	Glu	Glu	Ala	Phe	Phe	Arg	Gly	Val	Ser	Gln
		270					275					280
Gly	Arg	Gly	Gly	Leu	Gly	Ser	Ile	Phe	Val	Trp	Ala	Ser
				285					290			
Gly	Asn	Gly	Gly	Arg	Glu	His	Asp	Ser	Cys	Asn	Cys	Asp
	295					300					305	
Gly	Tyr	Thr	Asn	Ser	Ile	Tyr	Thr	Leu	Ser	Ile	Ser	Ser
			310					315				
Ala	Thr	Gln	Phe	Gly	Asn	Val	Pro	Trp	Tyr	Ser	Glu	Ala
320					325					330		
Cys	Ser	Ser	Thr	Leu	Ala	Thr	Thr	Tyr	Ser	Ser	Gly	Asn
		335					340					345
Gln	Asn	Glu	Lys	Gln	Ile	Val	Thr	Thr	Asp	Leu	Arg	Gln
				350					355			
Lys	Cys	Thr	Glu	Ser	His	Thr	Gly	Thr	Ser	Ala	Ser	Ala
	360					365					370	
Pro	Leu	Ala	Ala	Gly	Ile	Ile	Ala	Leu	Thr	Leu	Glu	Ala
			375					380				
Asn	Lys	Asn	Leu	Thr	Trp	Arg	Asp	Met	Gln	His	Leu	Val
385					390					395		
Val	Gln	Thr	Ser	Lys	Pro	Ala	His	Leu	Asn	Ala	Asn	Asp
		400					405					410
Trp	Ala	Thr	Asn	Gly	Val	Gly	Arg	Lys	Val	Ser	His	Ser
				415					420			
Tyr	Gly	Tyr	Gly	Leu	Leu	Asp	Ala	Gly	Ala	Met	Val	Ala
	425					430					435	
Leu	Ala	Gln	Asn	Trp	Thr	Thr	Val	Ala	Pro	Gln	Arg	Lys
			440					445				
Cys	Ile	Ile	Asp	Ile	Leu	Thr	Glu	Pro	Lys	Asp	Ile	Gly
450					455					460		
Lys	Arg	Leu	Glu	Val	Arg	Lys	Thr	Val	Thr	Ala	Cys	Leu
		465					470					475
Gly	Glu	Pro	Asn	His	Ile	Thr	Arg	Leu	Glu	His	Ala	Gln
				480					485			
Ala	Arg	Leu	Thr	Leu	Ser	Tyr	Asn	Arg	Arg	Gly	Asp	Leu
	490					495					500	

Ala	Ile	His	Leu	Val	Ser	Pro	Met	Gly	Thr	Arg	Ser	Thr	
			505					510					
Leu	Leu	Ala	Ala	Arg	Pro	His	Asp	Tyr	Ser	Ala	Asp	Gly	
515					520					525			
Phe	Asn	Asp	Trp	Ala	Phe	Met	Thr	Thr	His	Ser	Trp	Asp	
		530					535					540	
Glu	Asp	Pro	Ser	Gly	Glu	Trp	Val	Leu	Glu	Ile	Glu	Asn	
				545					550				
Thr	Ser	Glu	Ala	Asn	Asn	Tyr	Gly	Thr	Leu	Thr	Lys	Phe	
	555					560					565		
Thr	Leu	Val	Leu	Tyr	Gly	Thr	Ala	Pro	Glu	Gly	Leu	Pro	
			570					575					
Val	Pro	Pro	Glu	Ser	Ser	Gly	Cys	Lys	Thr	Leu	Thr	Ser	
580					585					590			
Ser	Gln	Ala	Cys	Val	Val	Cys	Glu	Glu	Gly	Phe	Ser	Leu	
		595					600					605	
His	Gln	Lys	Ser	Cys	Val	Gln	Asn	Cys	Pro	Pro	Gly	Phe	
				610					615				
Ala	Pro	Gln	Val	Leu	Asp	Thr	Asn	Tyr	Ser	Thr	Glu	Asn	
	620					625					630		
Asp	Val	Glu	Thr	Ile	Arg	Ala	Ser	Val	Cys	Ala	Pro	Cys	
			635					640					
His	Ala	Ser	Cys	Ala	Thr	Cys	Gln	Gly	Pro	Ala	Leu	Thr	
645					650					655			
Asp	Cys	Leu	Ser	Cys	Pro	Ser	His	Ala	Ser	Leu	Asp	Pro	
		660					665					670	
Val	Glu	Gln	Thr	Cys	Ser	Arg	Gln	Ser	Gln	Ser	Ser	Arg	
				675					680				
Glu	Ser	Pro	Pro	Gln	Gln	Gln	Pro	Pro	Arg	Leu	Pro	Pro	
	685					690					695		
Glu	Val	Glu	Ala	Gly	Gln	Arg	Leu	Arg	Ala	Gly	Leu	Leu	
			700					705					
Pro	Ser	His	Leu	Pro	Glu	Val	Val	Ala	Gly	Leu	Ser	Cys	
710					715					720			
Ala	Phe	Ile	Val	Leu	Val	Phe	Val	Thr	Val	Phe	Leu	Val	
		725					730					735	

Leu Gln Leu Arg Ser Gly Phe Ser Phe Arg Gly Val Lys
740 745

Val Tyr Thr Met Asp Arg Gly Leu Ile Ser Tyr Lys Gly
750 755 760

Leu Pro Pro Glu Ala Trp Gln Glu Glu Cys Pro Ser Asp
765 770

Ser Glu Glu Asp Glu Gly Arg Gly Glu Arg Thr Ala Phe
775 780 785

Ile Lys Asp Gln Ser Ala Leu End
790